

Complete Mitochondrial Genomes Confirm the Generic Placement of the Plateau Vole, *Neodon fuscus*

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Supporting Information

Table S1 Sequence data used in the design of primers.

Taxon	Accession number	Origin of specimen
<i>Microtus fortis fortis</i>	NC015241[1]	China: Ningxia
<i>Microtus fortis calamorum</i>	NC015243[1]	China: Hunan
<i>Microtus kikuchii</i>	NC003041[2]	China: Taipei
<i>Neodon irene</i>	NC016055[3]	China: Sichuan
<i>Microtus levis</i>	NC008064[4]	United States: Texas
<i>Proedromys liangshanensis</i>	NC013563[5]	China: Sichuan

Table S2 Mitochondrial genomes for Glires used in this study and their GenBank accession numbers.

Species	Common name	Accession number	Species Authority
<i>Alticola argentatus</i>	Silver Mountain Vole	DQ845186	Severtzov, 1879.
<i>Alticola barakshin</i>	Gobi Altai Mountain Vole	KJ556661[6]	Bannikov, 1947.
<i>Alticola macrotis</i>	Large-eared Mountain Vole	DQ845196	Radde, 1862.
<i>Apodemus chevrieri</i>	Chevrier's field mouse	NC017599[7]	Milne-Edwards, 1868
<i>Apodemus draco</i>	South China field mouse	NC019584	Barrett-Hamilton, 1900
<i>Arvicola terrestris</i>	European water vole	AF159400[8]	Amori, 1996
<i>Chionomys roberti</i>	Robert's Snow Vole	NC007936[9]	Satunin, 1903
<i>Cricetulus griseus</i>	Chinese hamster	NC007936	Milne-Edwards, 1867
<i>Cricetulus kamensis</i>	Tibetan dwarf hamster	NC024592[10]	Satunin, 1903
<i>Dicrostonyx groenlandicus</i>	Nearctic Collared Lemming	NC034313	Traill, 1823
<i>Dicrostonyx hudsonius</i>	Ungava Collared Lemming	NC034307	Pallas, 1778
<i>Dicrostonyx torquatus</i>	Palaearctic Collared Lemming	NC034646	Pallas, 1778
<i>Ellobius tancrei</i>	Eastern Mole Vole	AF119270	Blasius, 1884
<i>Eothenomys chinensis</i>	Sichuan red-backed vole	NC013571[11]	Thomas, 1891
<i>Eothenomys melanogaster</i>	Père David's Red-backed Vole	NC027418[12]	Milne-Edwards, 1871
<i>Lasiopodomys brandtii</i>	Brandt's Vole	JF906120	Radde, 1861
<i>Lasiopodomys mandarinus</i>	Mandarin vole	NC025283[13]	Milne-Edwards, 1871
<i>Lemmus trimucronatus</i>	Nearctic Brown Lemming	AF119276	Richardson, 1825
<i>Mesocricetus auratus</i>	Golden hamster	NC013276	Waterhouse, 1839
<i>Microtus fortis calamorum</i>	Yangtze vole	NC015243	Thomas, 1902
<i>Microtus fortis fortis</i>	Reed vole	NC015241	Bünchner, 1889
<i>Microtus kikuchii</i>	Taiwan vole	NC003041	Kuroda, 1920
<i>Microtus levis</i>	East European vole	NC008064	Miller, 1908
<i>Microtus ochrogaster</i>	Prairie Vole	NC027945	Wagner, 1842
<i>Mus musculus domesticus</i>	Western European house mouse	KF937873[14]	Linnaeus, 1758
<i>Mus musculus musculus</i>	Eastern European house mouse	NC010339[15]	Linnaeus, 1758
<i>Mus terricolor</i>	Earth-colored mouse	EU352649	Blyth, 1851
<i>Myodes glareolus</i>	Bank Vole	NC024538[16]	Schreber, 1780
<i>Myodes rufocanus</i>	Gray Red-backed Vole	NC029477[17]	Sundevall, 1846
<i>Myopus schisticolor</i>	Wood Lemming	AF119263	Lilljeborg, 1844
<i>Neodon clarkei</i>	Clarke's Vole	KP190221	Hinton, 1923
<i>Neodon irene</i>	Irene's mountain vole	NC016055	Thomas, 1911

<i>Neodon juldaschi</i>	Juniper Mountain Vole	EF599113	Severtzov, 1879
<i>Neodon leucurus</i>	Blyth's Mountain Vole	KP190225	Blyth, 1863
<i>Neodon linzhiensis</i>	unkown	HQ123618	Liu, 2012
<i>Neodon sikimensis</i>	Sikkim Mountain Vole	HQ123606	Horsfield, 1841
<i>Neodon sp.1 WJ-2014</i>	unkown	KP190217	Liu, 2014
<i>Niviventer excelsior</i>	Large white-bellited rat	NC019617[18]	Thomas, 1911
<i>Ochotona collaris</i>	Collared pika	NC003033[2]	Nelson, 1893
<i>Ochotona curzoniae</i>	Black-lipped pika	NC011029	Hodgson, 1858
<i>Petaurista hainana</i>	gaint flying squirrel	NC023089	G. Allen, 1925
<i>Proedromys liangshanensis</i>	Vole	NC013563	Liu, 2007
<i>Pteromys volans</i>	Siberian flying squirrel	NC019612[19]	Linnaeus, 1758
<i>Rattus norvegicus</i>	Norway rat	NC001665	Berkenhout, 1769
<i>Rattus rattus</i>	Black rat	NC012374[20]	Linnaeus, 1758
<i>Sciurus vulgaris</i>	Eurasian red squirrel	NC002369[21]	Linnaeus, 1758
<i>Synaptomys borealis</i>	Northern Bog Lemming	AF119259	Richardson, 1828
<i>Synaptomys cooperi</i>	Southern Bog Lemming	DQ323957[22]	Baird, 1857
<i>Tscherskia triton</i>	Greater long-tailed hamster	NC013068	de Winton, 1899

Table S3 Codon usage in the mitochondrial genome of *N. fuscus* with each value representing the total number and percentage of codons in all the 13 protein-coding genes.

Condon	Count (%)	Condon	Count (%)	Condon	Count (%)	Condon	Count (%)
UUU-Phe	60 (1.566)	UCU-Ser	68 (1.774)	UAU-Tyr	84 (2.192)	UGU-Cys	17 (0.444)
UUC-Phe	100 (2.609)	UCC-Ser	101 (2.636)	UAC-Tyr	74 (1.931)	UGC-Cys	20 (0.522)
UUA-Leu	88 (2.296)	UCA-Ser	125 (3.262)	UAA-Stop	75 (1.957)	UGA-Stop	67 (1.748)
UUG-Leu	22 (0.574)	UCG-Ser	30 (0.783)	UAG-Stop	47 (1.227)	UGG-Trp	17 (0.444)
CUU-Leu	65 (1.696)	CCU-Pro	112 (2.923)	CAU-His	77 (2.009)	CGU-Arg	15 (0.391)
CUC-Leu	84 (2.192)	CCC-Pro	85 (2.218)	CAC-His	87 (2.270)	CGC-Arg	18 (0.470)
CUA-Leu	155 (4.045)	CCA-Pro	122 (3.184)	CAA-Gln	101 (2.636)	CGA-Arg	26 (0.678)
CUG-Leu	43 (1.122)	CCG-Pro	20 (0.522)	CAG-Gln	46 (1.200)	CGG-Arg	9 (0.235)
AUU-Ile	107 (2.792)	ACU-Thr	85 (2.218)	AAU-Asn	71 (1.853)	AGU-Ser	25 (0.652)
AUC-Ile	106 (2.766)	ACC-Thr	82 (2.140)	AAC-Asn	99 (2.583)	AGC-Ser	56 (1.461)
AUA-Ile	123 (3.210)	ACA-Thr	143 (3.732)	AAA-Lys	96 (2.505)	AGA-Arg	15 (0.391)
AUG-Met	51 (1.331)	ACG-Thr	21 (0.548)	AAG-Lys	23 (0.600)	AGG-Arg	21 (0.548)
GUU-Val	24 (0.626)	GCU-Ala	46 (1.200)	GAU-Asp	33 (0.861)	GGU-Gly	19 (0.496)
GUC-Val	40 (1.044)	GCC-Ala	82 (2.140)	GAC-Asp	52 (1.357)	GGC-Gly	48 (1.253)
GUA-Val	48 (1.253)	GCA-Ala	53(1.383)	GAA-Glu	60 (1.566)	GGA-Gly	46 (1.200)
GUG-Val	24 (0.626)	GCG-Ala	15 (0.391)	GAG-Glu	27 (0.705)	GGG-Gly	30 (0.783)

Figure S1 Phylogenetic tree inferred from the 13 concatenated protein-coding genes from 33 species using ML analysis. The number at a node represents bootstrap value. ★ Indicates *N. fuscus* examined in our study. *Ochotona collaris* and *O. curzoniae* are used as outgroups.

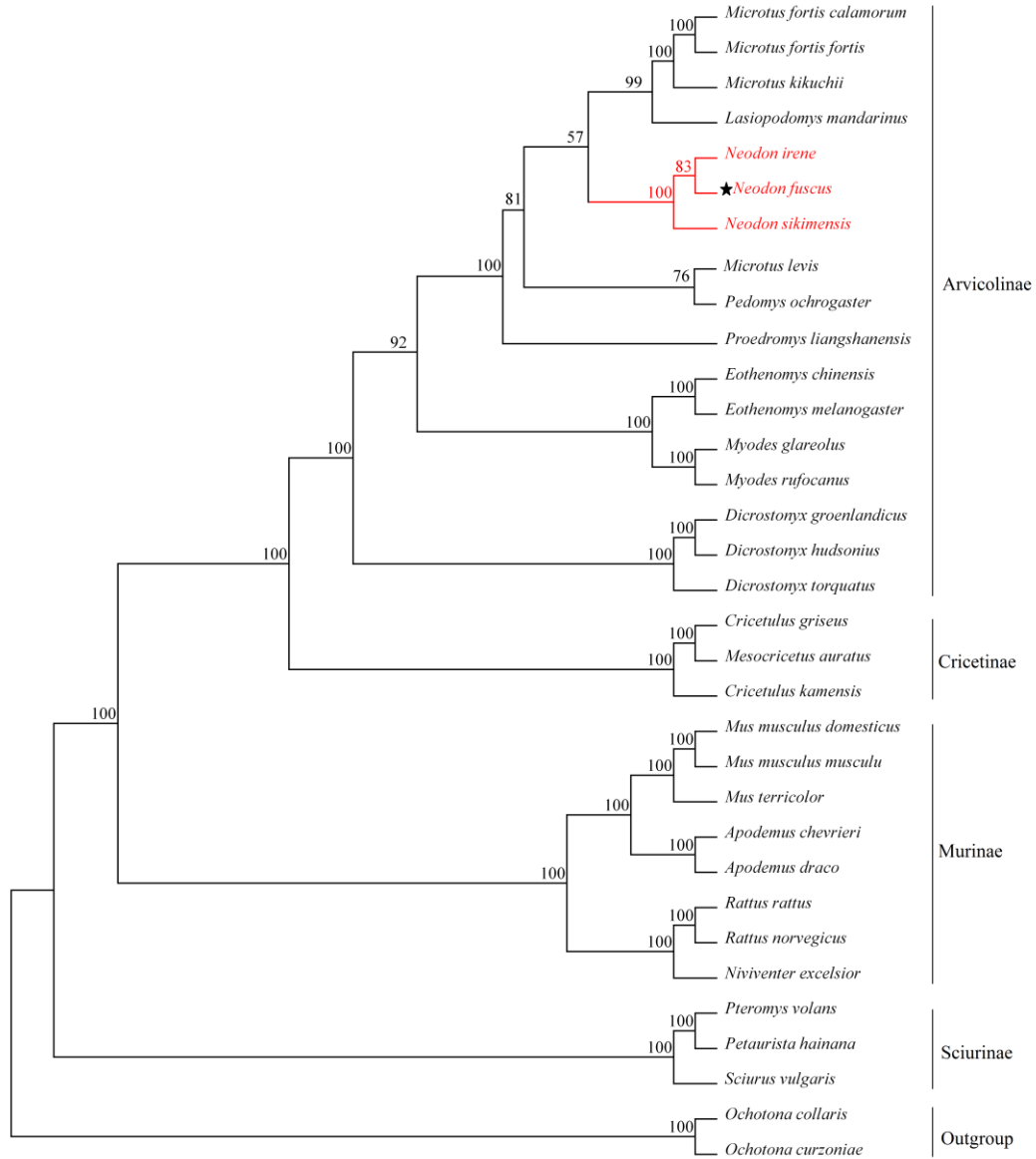
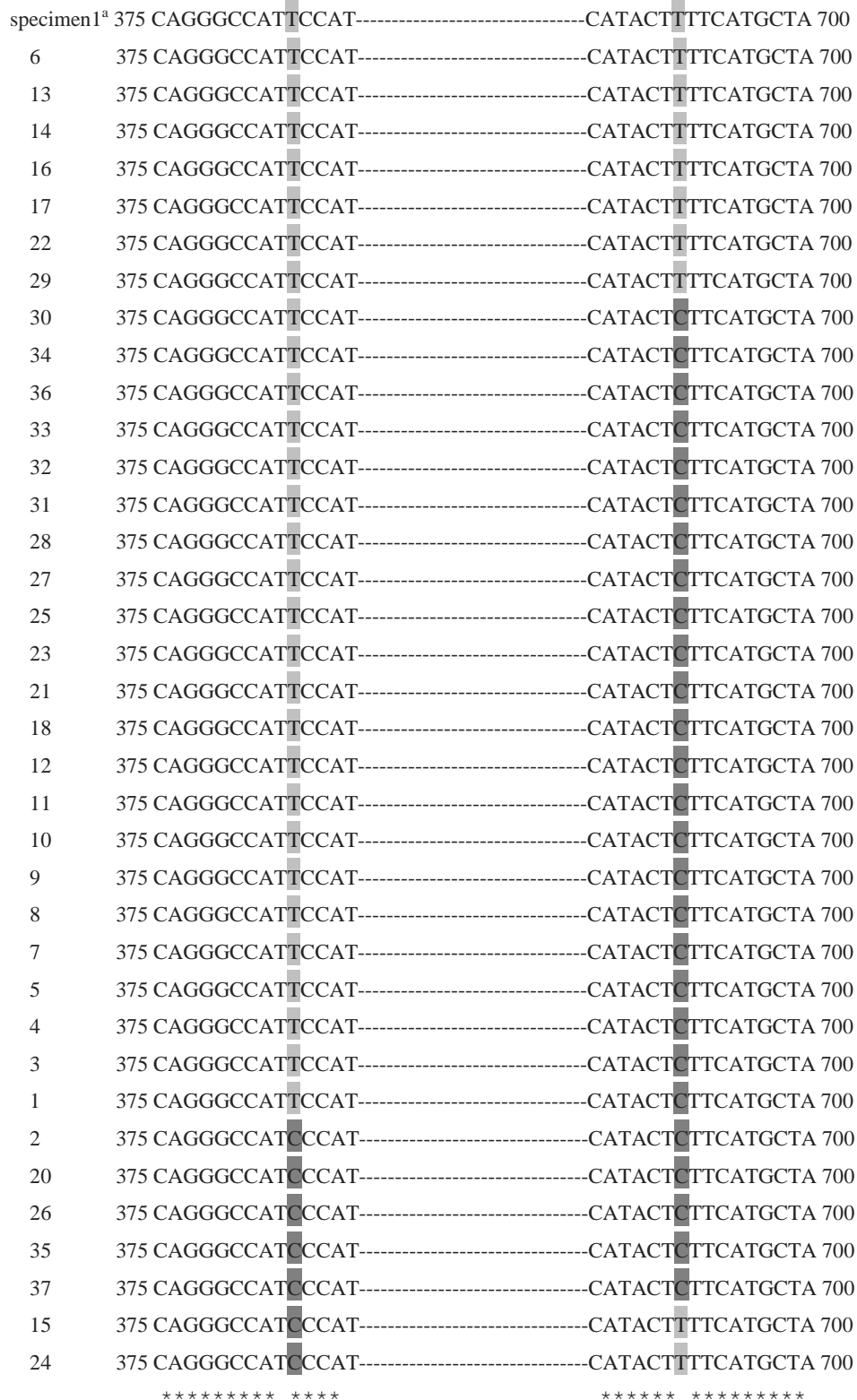


Figure S2 The multiple sequence alignment based on the D-loop region of 37 individuals of *N. fuscus*. Highlighted are the 384th and 691th bases are variable.



a: The specimen was used for sequencing of complete mtDNA in the study.

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